

A. Dec 10/01

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/147,443B

DATE: 01/25/2001  
TIME: 15:04:04

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3 <110> APPLICANT: Morell, Andreas
4      Imboden, Martin
5      Stadler, Beda
6      Miescher, Sylvia
7      Vogel, Monique
8      Amstutz, Hanspeter
10 <120> TITLE OF INVENTION: POLYPEPTIDES CAPABLE OF FORMING ANTIGEN BINDING
11      STRUCTURES WITH SPECIFICITY FOR THE RHESUS D ANTIGENS,
12      THE DNA ENCODING THEM AND THE PROCESS FOR THEIR
13      PREPARATION AND USE
15 <130> FILE REFERENCE: 6816/P63221US0
17 <140> CURRENT APPLICATION NUMBER: 09/147,443B
18 <141> CURRENT FILING DATE: 1999-01-21
20 <150> PRIOR APPLICATION NUMBER: PCT/EP97/03253
21 <151> PRIOR FILING DATE: 1997-06-20
23 <150> PRIOR APPLICATION NUMBER: EP 96810421.6
24 <151> PRIOR FILING DATE: 1996-06-24
26 <160> NUMBER OF SEQ ID NOS: 64
28 <170> SOFTWARE: PatentIn Ver. 2.1
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31 <211> LENGTH: 375
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
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37 <222> LOCATION: (1)..(375)
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42  1 5 10 15
44  tcc ctg aga ctc tcc tgt ata gcg tct gga ttc acc ctc agg aat tat 96
45  Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr
46  20 25 30
48  gcc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg 144
49  Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
50  35 40 45
52  gca ggt ata tgg ttt gat gga agt aac aaa aac tat gca gac tcc gtg 192
53  Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
54  50 55 60
56  aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat 240
57  Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
58  65 70 75 80
60  ctg caa ctg aac agc ctg aga gac gag gac acg gct gtg tat tat tgt 288
61  Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
62  85 90 95
64  gcg aga gag cga gca gca cgt ggt att tct agg ttc tat tac tac atg 336
65  Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met
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66          100          105          110          375
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70          115          120          125
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74 <211> LENGTH: 125
75 <212> TYPE: PRT
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80 1          5          10          15
82 Ser Leu Arg Leu Ser Cys Ile Ala Ser Gly Phe Thr Leu Arg Asn Tyr
83          20          25          30
85 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
86          35          40          45
88 Ala Gly Ile Trp Phe Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
89          50          55          60
91 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
92 65          70          75          80
94 Leu Gln Leu Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
95          85          90          95
97 Ala Arg Glu Arg Ala Ala Arg Gly Ile Ser Arg Phe Tyr Tyr Tyr Met
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116 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
117 1          5          10          15
119 gtc acc atc act tgc cgg gca agt cag agc att agg agc cat ttg aat 96
120 Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser His Leu Asn
121          20          25          30
123 tgg tat cag cag aaa cca ggg aaa gcc cct aag ttg ctg atc tat ggt 144
124 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
125          35          40          45
127 gcg tcc act ttg caa agt ggc gtc cca tca agg ttc agt ggc agt ggc 192
128 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
129          50          55          60
131 tct ggg gca gtt ttc act ctc acc atc gcc agt cta caa cct gaa gat 240
132 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
133 65          70          75          80
135 ttt gca act tac tac tgt caa gag agt tac agt aat cct cta atc acc 288

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136 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr
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140 Phe Gly Gln Gly Thr Arg Leu Glu Thr Lys
141                               100          105
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151   1                               5          10          15
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154                               20          25          30
156 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly
157   35          40          45
159 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
160   50          55          60
162 Ser Gly Ala Val Phe Thr Leu Thr Ile Ala Ser Leu Gln Pro Glu Asp
163   65          70          75          80
165 Phe Ala Thr Tyr Tyr Cys Gln Glu Ser Tyr Ser Asn Pro Leu Ile Thr
166   85          90          95
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169   100          105
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180 <222> LOCATION: (1)..(375)
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185   1                               5          10          15          48
187 tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc gcc ctc aga agt tct
188 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
189   20          25          30          96
191 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg
192 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
193   35          40          45          144
195 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg
196 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
197   50          55          60          192
199 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat
200 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
201   65          70          75          80          240
203 ctc caa atg cgc agt ctg agt gcc gac gac acg gct gtg tat tac tgt
204 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
205   85          90          95          100          105          110          115          120          125          130          135          140          145          150          155          160          165          170          175          180          185          190          195          200          205          210          215          220          225          230          235          240          245          250          255          260          265          270          275          280          285          290          295          300          305          310          315          320          325          330          335          340          345          350          355          360          365          370          375          288

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207 gcg aga gac aag gcg gtt cgg gga att agc agg tac aac tat tac atg
208 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
209          100          105          110          375
211 gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tca
212 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
213          115          120          125
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217 <211> LENGTH: 125
218 <212> TYPE: PRT
219 <213> ORGANISM: Homo sapiens
221 <400> SEQUENCE: 6
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223 1          5          10          15
225 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Ala Leu Arg Ser Ser
226          20          25          30
228 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
229          35          40          45
231 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
232          50          55          60
234 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr
235 65          70          75          80
237 Leu Gln Met Arg Ser Leu Ser Ala Asp Asp Thr Ala Val Tyr Tyr Cys
238          85          90          95
240 Ala Arg Asp Lys Ala Val Arg Gly Ile Ser Arg Tyr Asn Tyr Tyr Met
241          100          105          110
243 Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
244          115          120          125
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251 <213> ORGANISM: Homo sapiens
253 <220> FEATURE:
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255 <222> LOCATION: (1)..(318)
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259 Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
260 1          5          10          15
262 gtc acc atc act tgc cgg gca agt cag aac att atc cgc tat tta aat 96
263 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn
264          20          25          30
266 tgg tat cag cag aag cca ggg aaa gcc cct agg ctc ctg atc tat ggt 144
267 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
268          35          40          45
270 gcg tcc act ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga 192
271 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
272          50          55          60
274 tct ggg aca gat ttc act ctc acc atc agt agt ctg caa cct gaa gat 240

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275 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
276 65 70 75 80 288
278 ttt gca act tac tac tgt caa cag agt tac cgt acc cct cca ttc act
279 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
280 85 90 95 318
282 ttc ggc cct ggg acc aaa gtg gag atc aaa
283 Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
284 100 105
287 <210> SEQ ID NO: 8
288 <211> LENGTH: 106
289 <212> TYPE: PRT
290 <213> ORGANISM: Homo sapiens
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294 1 5 10 15
296 Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Ile Arg Tyr Leu Asn
297 20 25 30
299 Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile Tyr Gly
300 35 40 45
302 Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
303 50 55 60
305 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
306 65 70 75 80
308 Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Pro Phe Thr
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317 <211> LENGTH: 375
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319 <213> ORGANISM: Homo sapiens
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323 <222> LOCATION: (1)..(375)
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326 cag gtg aaa ctg ctc gag tct ggg gga ggc gtg gtc cag ccg ggg ggg 48
327 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
328 1 5 10 15
330 tcc ctg aga ctc tcc tgt gaa gcg tct gga ttc acc ctc aga agt tct 96
331 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Leu Arg Ser Ser
332 20 25 30
334 ggc atg cac tgg gtc cgc cag gct cct ggc aag ggg ctg gag tgg gtg 144
335 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
336 35 40 45
338 gca ctt ata tgg ttt gat gga agt atc aga tcg tat gca gaa tcc gtg 192
339 Ala Leu Ile Trp Phe Asp Gly Ser Ile Arg Ser Tyr Ala Glu Ser Val
340 50 55 60
342 aag ggc cga ttc acc atc tcc aga gac act tcc aag aac acc cta tat 240
343 Lys Gly Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Leu Tyr

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VERIFICATION SUMMARY  
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